

## General information

Entry name	ATPG_HAEIN
Accession number	<u>P43716</u>
Created	Rel. 32, 1-NOV-1995
Sequence update	Rel. 32, 1-NOV-1995
Annotation update	Rel. 40, 16-OCT-2001

## Description and origin of the Protein

Description	ATP SYNTHASE GAMMA CHAIN (EC <u>3.6.3.14</u> ).
Gene name(s)	ATPG OR HI0480.
Organism source	Haemophilus influenzae.
Taxonomy	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus.
NCBI TaxID	<u>727</u>

## References

[1] Fleischmann,R.D., Adams,M.D., White,O., Clayton,R.A., Kirkness,E.F., Kerlavage,A.R., Bult,C.J., Tomb,J.-F., Dougherty,B.A., Merrick,J.M., McKenney,K., Sutton,G., Fitzhugh,W., Fields,C.A., Gocayne,J.D., Scott,J.D., Shirley,R., Liu,L.-I., Glodek,A., Kelley,J.M., Weidman,J.F., Phillips,C.A., Spriggs,T., Hedblom,E., Cotton,M.D., Utterback,T.R., Hanna,M.C., Nguyen,D.T., Saudek,D.M., Brandon,R.C., Fine,L.D., Fritchman,J.L., Fuhrmann,J.L., Geoghagen,N.S.M., Gnehm,C.L., McDonald,L.A., Small,K.V., Fraser,C.M., Smith,H.O., Venter,J.C.,  
Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
(1995) *Science* **269**:496

Position SEQUENCE FROM N.A.

Comments	STRAIN=RD / KW20 / ATCC 51907;
Medline	<u>95350630</u>
PubMed	<u>7542800</u>

### Comments

#### FUNCTION

PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.

#### SUBUNIT

F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

#### SIMILARITY

BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.

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## Database cross-references

EMBL	<a href="#">U32730</a> ; <a href="#">AAC22138.1</a> ; -.
HSSP	<a href="#">P05631</a> ; <a href="#">1BMF</a> .
TIGR	<a href="#">HI0480</a> ; -.
InterPro	<a href="#">IPR000131</a> ; ATPase_gamma.
Pfam	<a href="#">PF00231</a> ; ATP-synt; 1.
PRINTS	<a href="#">PRO0126</a> ; ATPASEGAMMA.
PROSITE	<a href="#">PS00153</a> ; ATPASE_GAMMA; 1.

## Keywords

[ATP synthesis](#); [CF\(1\)](#); [Hydrogen ion transport](#); [Hydrolase](#); [Complete proteome](#);

## Sequence information

Length: 289 aa, molecular weight: 32069 Da, CRC64 checksum:

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[General](#) [Description](#) [References](#) [Comments](#) [Links](#) [Keywords](#) [Sequence](#)

## ATP synthase gamma subunit

Accession	IPR000131: (ATPase_gamma) matches 100 proteins
FullName	ATP synthase gamma subunit
Type	Domain
Signatures	PRINTS: <a href="#">PRO0126 ATPASEGAMMA</a> PROSITE: <a href="#">PS00153 ATPASE_GAMMA</a> PFAM: <a href="#">PF00231 ATP-synt</a>
Molecular Function	hydrogen-transporting two-sector ATPase ( <a href="#">GO:0003936</a> )
Biological Process	hydrogen transport ( <a href="#">GO:0006818</a> )
Cellular Component	membrane ( <a href="#">GO:0016020</a> )
Abstract	ATP synthase (proton-translocating ATPase) [EC: <a href="#">3.6.1.34</a> ] [1, 2] is a component of the cytoplasmic membrane of eubacteria, the inner membrane of mitochondria, and the thylakoid membrane of chloroplasts. The ATPase complex is composed of an oligomeric transmembrane sector, called CF(0), and a catalytic core, called coupling factor CF(1). The former acts as a proton channel; the latter is composed of five subunits, alpha, beta, gamma, delta and epsilon. Subunit gamma is believed to be important in regulating ATPase activity and the flow of protons through the CF(0) complex. The best conserved region of the gamma subunit [3] is its C-terminus which seems to be essential for assembly and catalysis.
Examples	<a href="#">P36542</a> <a href="#">P00837</a> <a href="#">P29790</a>
	<a href="#">View Signature matches on the examples</a>
	1. Futai,M., Noumi,T., Maeda,M., ATP synthase (H <sup>+</sup> -ATPase) - Results by combined

<b>References</b>	<p>biochemical and molecular biological approaches. (1989) <i>Annu. Rev. Biochem.</i> <b>58</b>: 111-136 [MEDLINE:<a href="#">89372792</a>] [PUB00000063]</p> <p>2. Senior,A.E., ATP synthesis by oxidative phosphorylation. (1988) <i>Physiol. Rev.</i> <b>68</b>: 177-231 [MEDLINE:<a href="#">88097736</a>] [PUB00004515]</p> <p>3. Futai,M., Maeda,M., Miki,J., Mukohata,Y., The gamma-subunit of ATP synthase from spinach chloroplasts - primary structure deduced from the cloned cDNA sequence. (1988) <i>FEBS Lett.</i> <b>232</b>: 221-226 [MEDLINE:<a href="#">88211863</a>] [PUB00001558]</p>
<b>Database links</b>	<p>BLOCKS:<a href="#">IPB000131</a>; PDOC:<a href="#">PDOC00138</a>;</p>
<b>Matches</b>	<p><a href="#">Table</a> <a href="#">all</a> <a href="#">Graphical</a> <a href="#">all</a></p>

1. *Science*. 1995, 269 (5223):496-512

Related Articles by NCBI

## Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

Fleischmann, R D. , Adams, M D. , White, O. , Clayton, R A. , Kirkness, E F. ,  
Kerlavage, A R. , Bult, C J. , Tomb, J F. , Dougherty, B A. , Merrick, J M.

Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.

An approach for genome analysis based on sequencing and assembly of unselected pieces of DNA from the whole chromosome has been applied to obtain the complete nucleotide sequence (1,830,137 base pairs) of the genome from the bacterium *Haemophilus influenzae* Rd. This approach eliminates the need for initial mapping efforts and is therefore applicable to the vast array of microbial species for which genome maps are unavailable. The *H. influenzae* Rd genome sequence (Genome Sequence DataBase accession number L42023) represents the only complete genome sequence from a free-living organism.

MedlineID: 95350630

PMID: 7542800

ISSN: 0036-8075

Publication Type:

Journal Article

Substances:

Bacterial Proteins

DNA, Bacterial

RNA, Bacterial

RNA, Ribosomal

1. *Science*. 1995, 269 (5223):496-512

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MedlineID: 95350630

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Substances:

Bacterial Proteins

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RNA, Bacterial

RNA, Ribosomal

ID AR089428 standard; DNA; UNC; 1374 BP.  
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 AC AR089428;  
 XX  
 SV AR089428.1  
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 DT 12-SEP-2000 (Rel. 65, Last updated, Version 1)  
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 DE Sequence 187 from patent US 5994066.  
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 OS unidentified  
 OC unclassified.  
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 RN [1]  
 RP 1-1374  
 RA Bergeron M.G., Picard F.J., Ouellette M., Roy P.H.;  
 RT "Species-specific and universal DNA probes and amplification primers to  
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 RT antibiotic resistance genes from clinical specimens for routine diagnosis  
 RT in microbiology laboratories";  
 RL Patent number US5994066-A/187, 30-NOV-1999.  
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DT 15-JUN-1998 (Rel. 56, Last updated, Version 9)  
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DE Haemophilus influenzae Rd section 45 of 163 of the complete genome.  
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KW .  
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OS Haemophilus influenzae Rd  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus;  
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RA Kerlavage A.R., Bult C.J., Tomb J., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F.,  
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RA Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D.,  
RA Fritchman J.L., Fuhrmann J.L., Geoghegan N.S., Gnehm C.L., McDonald L.A.,  
RA Small K.V., Fraser C.M., Smith H.O., Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd";  
RL Science 269(5223):496-512(1995).  
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RP 1-13828  
RX MEDLINE; 96398784.  
RA Tatusov R.L., Mushegian A.R., Bork P., Brown N.P., Hayes W.S.,  
RA Borodovsky M., Rudd K.E., Koonin E.V.;  
RT "Metabolism and evolution of Haemophilus influenzae deduced from a  
RT whole-genome comparison with Escherichia coli";  
RL Curr. Biol. 6(3):279-291(1996).  
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RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;  
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RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD  
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RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD  
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RA Hickey E., Dodson R., Gwinn M.;  
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RL Submitted (28-MAY-1998) to the EMBL/GenBank/DDBJ databases.  
RL The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD  
RL 20850, USA  
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DR SWISS-PROT; O86225; Y48A\_HAEIN.  
 DR SWISS-PROT; P43714; ATPA\_HAEIN.  
 DR SWISS-PROT; P43715; ATPB\_HAEIN.  
 DR SWISS-PROT; P43716; ATPG\_HAEIN.  
 DR SWISS-PROT; P43717; ATPD\_HAEIN.  
 DR SWISS-PROT; P43718; ATPE\_HAEIN.  
 DR SWISS-PROT; P43719; ATP6\_HAEIN.  
 DR SWISS-PROT; P43720; ATPF\_HAEIN.  
 DR SWISS-PROT; P43721; ATPL\_HAEIN.  
 DR SWISS-PROT; P44002; Y476\_HAEIN.  
 DR SWISS-PROT; P44327; HIS7\_HAEIN.  
 DR SWISS-PROT; P44340; HIS5\_HAEIN.  
 DR SWISS-PROT; P44423; HIS8\_HAEIN.  
 DR SWISS-PROT; P44434; HIS2\_HAEIN.  
 DR SWISS-PROT; P44435; HIS4\_HAEIN.  
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 RL Diagnostic Medicine/Pathobiology, Kansas State University, 1800 Denison  
 RL Ave, Manhattan, KS 66506-5605, USA  
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